



PATENT
Attorney Docket: 53356-5001-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: **G. Lenzen *et al.***)
)
Application No. **09/319,724**)
)
Filed: **September 8, 1999**)
)
For: **MAMMALIAN ICYP**)
 (IODOCYANOPINDOLOL) RECEPTOR)
 AND ITS APPLICATIONS)

Group Art Unit: 1646

Examiner: **Michael T. Brannock**

RECEIVED

JUL 28 2003

Commissioner for Patents
Washington, D.C. 20231

TECH CENTER 1600/2900

DECLARATION UNDER 37 CFR §1.132 BY TOSHINARI SUGASAWA

I, Toshinari Sugasawa, declare as follows:

1. I am a co-inventor of the subject matter described and claimed in the above-referenced patent application, U.S. Patent Application No. 09/319,724. A bibliography of relevant publications and my curriculum vitae are attached hereto.
2. I have read and understand the non-final Office Action (paper no. 16) that was mailed March 24, 2003, in the above-referenced application, including the rejection for lack of enablement under 35 U.S.C. §112, first paragraph. It is my understanding that the basis for the rejection is that the specification, while being enabled for polynucleotides encoding a protein of SEQ ID No. 14 and the portion thereof capable of binding ICYP, allegedly fails to provide sufficient guidance for polypeptides that are not 100% identical to SEQ ID No. 14, *i.e.*, substitutions, deletions and insertions, but which still retain a desired property of the polypeptide of SEQ ID No. 14.
3. The specification reports the identification and cloning of the human ICYP receptor following the identification of a human expressed sequence tag (EST) using the tBLASTn program. The human fragment was identified based on homology with a highly conserved

formic acid cleaved fragment of the rat protein (SEQ ID No. 6), which demonstrated almost 100% homology to the corresponding human sequence identified (SEQ ID No. 5) (see Example 3 starting on page 32).

This suggests that this family of proteins is highly conserved across species, and that the same, well known methodology used to clone the human gene could also be used without undue experimentation to clone natural variants from other species.

4. In line with the methodology reported in Example 3 of the specification, this declaration describes the results of tBLASTn database searches using the fragments represented by SEQ ID Nos. 5 and 6. As shown in the attached tBLASTn results, when conducted with the amino acid sequence of SEQ ID No. 5, the search revealed 14 clones showing 100% homology in the region of the fragment represented by SEQ ID No. 5. Most all of these clones reveal homologous animal ICYP receptors, including the receptor from human, mouse, *C. elegans*, zebra fish, etc. (Note that TM9SF3 (transmembrane protein 9 superfamily member 3) and SMBP (SM-11044 binding protein) and ICYP receptor are the same protein.)

5. When the tBLASTn search was conducted with the amino acid sequence of SEQ ID No. 6, which comprises an "X" in the amino acid sequence of the formic acid cleaved fragment, 16 clones were identified including chicken and fruit fly TM9SF3. Thus, the fragment used in Example 3 of the specification to identify human ICYP receptor cDNA using the tBLASTn program could also be used in the same manner to identify natural variants from other species. Furthermore, clones corresponding to the identified sequences could be readily isolated by one of skill in the art using the methodology outlined in Example 3.

6. I further declare that all statements made herein of my own knowledge are true, and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

By: 蒙采敏成

Dated: 9 July 2003

CURRICULUM VITAE

Name: Toshinari Sugasawa, Ph.D.
Sex: Male
Date of birth: 29 December, 1959
Place of birth: Tokyo, Japan
Marital status: Married
Nationality: Japanese
Present address: Discovery Research Laboratories II, Research Division,
Sumitomo Pharmaceuticals Co., Ltd.
3-1-98, Kasugade Naka 3-Chome, Konohana-ku,
Osaka 554-0022, Japan
Phone: (81)6(6466)5269
Fax: (81)6(6466)5182
Home address: 8-35-607, Wakayama-cho, Nishinomiya-shi,
Hyogo 663-8016, Japan
Phone: (81)798(63)6075
Fax: (81)798(63)6075

Education:

1992-1996 Institut Cochin de Génétique Moléculaire,
Laboratoire d'Immuno-Pharmacologie Moléculaire, CNRS-UPR 0415
and
Unités de Formation et de Recherche - Biochimie,
Université Paris VII

Awarded the Doctor of Science for a thesis entitled "Caractérisation Pharmacologique, Biochimique et Immuno-chimique d'une Nouvelle Protéine Liant l'Iodocyanopindolol: "ICYPBP".

Concentrations: Purification, amino-acid sequencing and cDNA cloning of a novel membrane protein. Transfection of the plasmid DNA into the mammalian host cells. Pharmacological and biochemical analysis of the transfectants.

Professor: Dr. A. Donny Strosberg

1979-1983 Department of Animal Science, Faculty of Agriculture,
Kyoto University

Awarded the Bachelor's Degree, Science in Agriculture for a thesis
entitled "In vitro fertilization of Mongolian Gerbill eggs".

Concentrations: Study of the suitable culture medium composition for
in vitro fertilization of mammalian eggs.

Professor: Dr. Akira Iritani

Research and professional experience:

1983-1992 Research fellow at the Department of Pharmacology, Research
Laboratories, Sumitomo Pharmaceuticals Co., Ltd., working on the
pharmacological studies of phenylethanolamine-derivatives and
anti-asthmatic/allergic agents.

1997-present Senior Research Scientist at the Discovery Research Laboratories II,
Research Division, Sumitomo Pharmaceuticals Co., Ltd., working on
the pharmacological studies of anti-asthmatic/allergic agents.

Publications

- 1) Sugasawa T., Lenzen G., Simon S., Hidaka J., Cahen A., Guillaume J.-L., Camoin L., Strosberg A. D. and Nahmias C., The iodocyanopindolol and SM-11044 binding protein belongs to the TM9SF multispinning membrane protein superfamily., *Gene*. 273: 227-37 (2001)
- 2) Sugasawa T., Matsuzaki-Fujita M., Guillaume J.L., Camoin L., Morooka S. and Strosberg A. D., Characterization of a novel iodocyanopindolol and SM-11044 binding protein, which may mediate relaxation of depolarized rat colon tonus., *Journal of Biological Chemistry*. 272:21244-52 (1997)
- 3) Sugasawa, T. and Morooka S., Existence of Atypical β -Adrenoceptor on Guinea-pig Eosinophil., in Recent Advances in Cellular and Molecular Biology (Wegmann, R.J. and Wegmann, M.A., eds) Vol.3, pp 223-227, Peeters Press, Leuven, Belgium (1992)

- 4) Sugasawa T. and Morooka S., Effect of BRL-35135 on LTB₄-induced guinea pig eosinophil chemotaxis., *Agents & Actions*. 37:232-7 (1992)
- 5) Sugasawa T., Matsuzaki M., Morooka S., Foignant N., Blin N. and Strosberg A. D., In vitro study of a novel atypical beta-adrenoceptor agonist, SM-11044., *European Journal of Pharmacology*. 216:207-15 (1992)
- 6) Sugasawa T., Imanishi N. and Morooka S., Effect of the selective PAF antagonist SM-10661 on an asthmatic model. 2. Effect on antigen-induced dual asthmatic response and infiltration of leukocytes into airways in actively sensitized conscious guinea pigs., *Lipids*. 26:1305-9 (1991)
- 7) Uchida M., Imanishi N., Sugasawa T. and Morooka S., Effect of the selective PAF antagonist SM-10661 on an asthmatic model. 1. Effect on passive anaphylactic bronchoconstriction in guinea pigs., *Lipids*. 26:1301-4 (1991)



translating

BLAST

Nucleotide

Protein

Translations

Retrieve results for an
RID

Search

DPSFFQHRHWFSIFNS

Choose a translation PROTEIN query - TRANSLATED database [tblastn]

Set subsequence From: To:

Choose database nr

Genetic codes Disabled

Now: **BLAST** or **Reset query** **Reset all**

Options for advanced blasting

Limit by entrez query or select from: (none)

Choose filter ☒ Low complexity ☐ Mask for lookup table only ☐ Mask lower case

Expect 10

Word Size 3

Matrix BLOSUM62 Gap Costs Existence: 11 Extension: 1

Other advanced

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Limit results by entrez query or select from: (none)

Expect value range:

Layout: Two Windows Formatting options on page with results: None

Autoformat Semi-auto



results of BLAST

TBLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs". Nucleic Acids Res. 25:3389-3402.

RID: 1054277721-021460-25890

Query=

(17 letters)

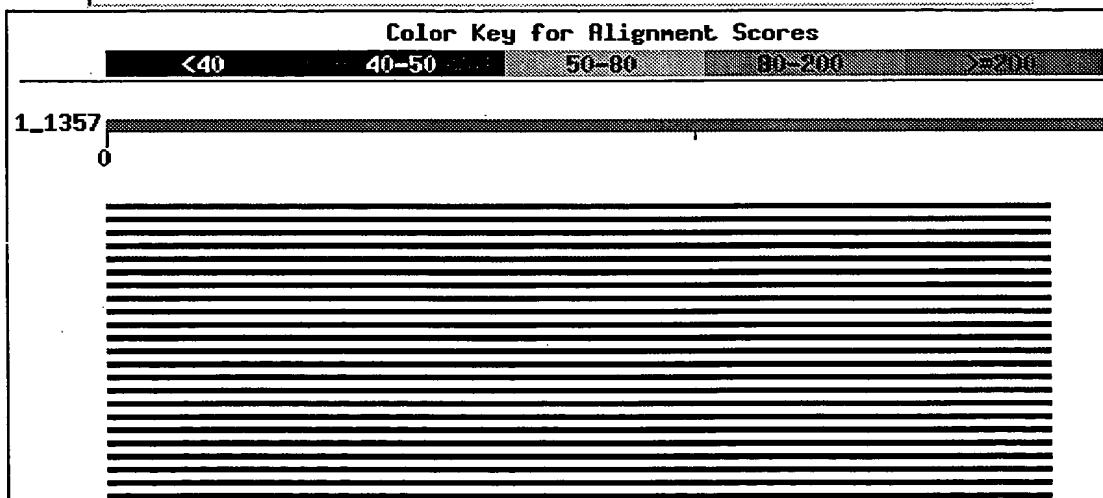
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,772,460 sequences: 8,313,506,101 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)











Taxonomy reportsDistribution of 23 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

	Score (bits)	E Value	
gi 9755050 gb AF269150.1 AF269150 Homo sapiens transmembran...	43	0.008	LU
gi 9755048 gb AF269149.1 AF269149 Gallus gallus transmembra...	43	0.008	
gi 30026031 ref NM_178146.1 Mus musculus RIKEN cDNA 181007...	43	0.008	L
gi 26344651 dbj AK075807.1 Mus musculus 10 day old male pa...	43	0.008	L
gi 22760523 dbj AK074824.1 Homo sapiens cDNA FLJ90343 fis...	43	0.008	L
gi 6650721 gb AF116347.1 AF116347 Homo sapiens SM-11044 bin...	43	0.008	LU
gi 17543267 ref NM_067729.1 Caenorhabditis elegans transme...	43	0.008	L
gi 14042725 dbj AK027788.1 Homo sapiens cDNA FLJ14882 fis...	43	0.008	LU
gi 19111161 ref NM_133352.1 Mus musculus RIKEN cDNA 181007...	43	0.008	LU
gi 13435914 gb BC004799.1 Mus musculus RIKEN cDNA 1810073M...	43	0.008	LU
gi 28278504 gb BC046021.1 Danio rerio, Similar to expresse...	43	0.008	
gi 9755052 gb AF269151.1 AF269151 Mus musculus transmembran...	43	0.008	LU
gi 7021041 dbj AK000756.1 Homo sapiens cDNA FLJ20749 fis...	43	0.008	LU



gi 18088072 gb BC020959.1 BC020959	Homo sapiens, clone MGC:...	43	0.008	 
gi 24658498 ref NM_139722.2 	Drosophila melanogaster CG1059...	42	0.017	
gi 17945956 gb AY071401.1 	Drosophila melanogaster RE48767 ...	42	0.017	 
gi 30681999 ref NM_100970.2 	Arabidopsis thaliana endomembr...	35	2.7	
gi 17933309 gb AF446365.1 AF446365	Arabidopsis thaliana At1...	35	2.7	
gi 20148414 gb AY081536.1 	Arabidopsis thaliana endomembran...	35	2.7	
gi 15810406 gb AY056242.1 	Arabidopsis thaliana putative en...	35	2.7	
gi 30793946 gb BT008600.1 	Arabidopsis thaliana clone U1129...	35	2.7	
gi 15451171 gb AY054666.1 	Arabidopsis thaliana endomembran...	35	2.7	
gi 17380901 gb AY063907.1 	Arabidopsis thaliana putative en...	35	2.7	

Alignments

Get selected sequences

Select all

Deselect all

☐ [gi|9755050|gb|AF269150.1|AF269150](#)  Homo sapiens transmembrane protein TM9SF3 (TM9SF3) mRNA, complete cds
Length = 3592


Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +2

Query: 1 DPSFFQHRHWFNFIENS 17
DPSFFQHRHWFNFIENS
Sbjct: 854 DPSFFQHRHWFNFIENS 904

☐ [gi|9755048|gb|AF269149.1|AF269149](#) Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds
Length = 234


Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +1

Query: 1 DPSFFQHRHWFNFIENS 17
DPSFFQHRHWFNFIENS
Sbjct: 112 DPSFFQHRHWFNFIENS 162

☐ [gi|30026031|ref|NM_178146.1|](#)  Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
Length = 1155


Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +1

Query: 1 DPSFFQHRHWFNFIENS 17
DPSFFQHRHWFNFIENS
Sbjct: 631 DPSFFQHRHWFNFIENS 681

☐ [gi|26344651|dbj|AK075807.1|](#)  Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810073M23 product:unknown EST, full insert sequence
Length = 2479



Score = 43.1 bits (100), Expect = 0.008
Identities = 17/17 (100%), Positives = 17/17 (100%)
Frame = +2

Query: 1 DPSFFQHRHWFNFIENS 17
DPSFFQHRHWFNFIENS
Sbjct: 749 DPSFFQHRHWFNFIENS 799

☐ [gi|22760523|dbj|AK074824.1|](#)  Homo sapiens cDNA FLJ90343 fis, clone NT2RP2002824, weakly similar to ENDOSOMAL P24A PROTEIN PRECURSOR
Length = 2864

Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 145 DPSFFQHRHHWFSIFNS 195

 [gi|6650721|gb|AF116347.1|AF116347](#)  Homo sapiens SM-11044 binding protein mRNA, partial cds
 Length = 1804



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 604 DPSFFQHRHHWFSIFNS 654

 [gi|17543267|ref|NM_067729.1|](#)  Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA
 Length = 1743

Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 610 DPSFFQHRHHWFSIFNS 660

 [gi|14042725|dbj|AK027788.1|](#)  Homo sapiens cDNA FLJ14882 fis, clone PLACE1003537, weakly similar to ENDOSOMAL P24A PROTEIN PRECURSOR
 Length = 2459



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +3

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 510 DPSFFQHRHHWFSIFNS 560

 [gi|19111161|ref|NM_133352.1|](#)  Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik), mRNA
 Length = 3143


Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 713 DPSFFQHRHHWFSIFNS 763

 [gi|13435914|gb|BC004799.1|](#)  Mus musculus RIKEN cDNA 1810073M23 gene, mRNA (cDNA clone MGC:8136 IMAGE:3589474), complete cds
 Length = 2848



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 DPSFFQHRHHWFSIFNS
 Sbjct: 410 DPSFFQHRHHWFSIFNS 460

 [gi|28278504|gb|BC046021.1|](#) Danio rerio, Similar to expressed sequence AW146116, clone MGC:56246 IMAGE:5601580, mRNA, complete cds
 Length = 2082



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 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

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 Sbjct: 725 DPSFFQHRHHWFSIFNS 775

 >[gi|9755052|gb|AF269151.1|AF269151](#)  Mus musculus transmembrane protein TM9SF3 (Tm9sf3) mRNA, complete cds
 Length = 3143



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

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 Sbjct: 713 DPSFFQHRHHWFSIFNS 763

 >[gi|7021041|dbj|AK000756.1](#)  Homo sapiens cDNA FLJ20749 fis, clone HEP05301
 Length = 2973



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

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 Sbjct: 257 DPSFFQHRHHWFSIFNS 307

 >[gi|18088072|gb|BC020959.1|BC020959](#)  Homo sapiens, clone MGC:8842 IMAGE:3850015, mRNA, complete cds
 Length = 2870



Score = 43.1 bits (100), Expect = 0.008
 Identities = 17/17 (100%), Positives = 17/17 (100%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
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 Sbjct: 434 DPSFFQHRHHWFSIFNS 484

 >[gi|24658498|ref|NM_139722.2](#)  Drosophila melanogaster CG10590-PA [Drosophila melanogaster]
 (CG10590) mRNA, complete cds
 Length = 2663


Score = 42.0 bits (97), Expect = 0.017
 Identities = 16/17 (94%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DP+FFQHRHHWFSIFNS
 Sbjct: 823 DPNFFQHRHHWFSIFNS 873

 >[gi|17945956|gb|AY071401.1](#)  Drosophila melanogaster RE48767 full length cDNA
 Length = 2662

Score = 42.0 bits (97), Expect = 0.017
 Identities = 16/17 (94%), Positives = 17/17 (100%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 DP+FFQHRHHWFSIFNS
 Sbjct: 823 DPNFFQHRHHWFSIFNS 873

 >[gi|30681999|ref|NM_100970.2](#) Arabidopsis thaliana endomembrane protein 70, putative (Atlg10950)
 mRNA, complete cds
 Length = 2238

Score = 34.7 bits (78), Expect = 2.7

Identities = 13/17 (76%), Positives = 17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 740 DYPFFEHHQHHWFSIFNS 790

>gi|17933309|gb|AF446365.1|AF446365 Arabidopsis thaliana Atlg10950/T19D16_13 mRNA, complete cds
 Length = 2094

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 740 DYPFFEHHQHHWFSIFNS 790

>gi|20148414|gb|AY081536.1| Arabidopsis thaliana endomembrane protein EMP70 precursor isolog
 (Atlg10950) mRNA, complete cds
 Length = 1888

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 634 DYPFFEHHQHHWFSIFNS 684

>gi|15810406|gb|AY056242.1| Arabidopsis thaliana putative endomembrane protein EMP70 precursor
 isolog (Atlg10950) mRNA, partial cds
 Length = 1650

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +2

Query: 1 DPSFFQHRHHWFSIFNS 17
 D FF+H+HHWFSIFNS
 Sbjct: 251 DYPFFEHHQHHWFSIFNS 301

>gi|30793946|gb|BT008600.1| Arabidopsis thaliana clone U11293 putative endomembrane protein 70
 (Atlg10950) mRNA, complete cds
 Length = 1966

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +1

Query: 1 DPSFFQHRHHWFSIFNS 17
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>gi|15451171|gb|AY054666.1| Arabidopsis thaliana endomembrane protein EMP70 precursor isolog
 (Atlg10950: T19D16.13) mRNA, complete cds
 Length = 2062

Score = 34.7 bits (78), Expect = 2.7
 Identities = 13/17 (76%), Positives = 15/17 (88%)
 Frame = +3

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 D FF+H+HHWFSIFNS
 Sbjct: 693 DYPFFEHHQHHWFSIFNS 743

>gi|17380901|gb|AY063907.1| Arabidopsis thaliana putative endomembrane protein EMP70 precursor
 isolog (Atlg10950) mRNA, complete cds
 Length = 2113

Score = 34.7 bits (78), Expect = 2.7
Identities = 13/17 (76%), Positives = 15/17 (88%)
Frame = +3

Query: 1 DPSFFQHRHWFHIFNS 17
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Sbjct: 717 DYPFFEHQHWFHIFNS 767

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: May 30, 2003 12:03 AM

Number of letters in database: 276,428,487

Number of sequences in database: 1,772,460

Lambda	K	H
0.337	0.144	0.553

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 258,839,836

Number of Sequences: 1772460

Number of extensions: 955261

Number of successful extensions: 13875

Number of sequences better than 10.0: 23

Number of HSP's better than 10.0 without gapping: 13550

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 13873

length of query: 17

length of database: 2,771,168,700

effective HSP length: 0

effective length of query: 24

effective length of database: 2,771,168,700

effective search space: 66508048800

effective search space used: 66508048800

frameshift window, decay const: 50, 0.1

T: 13

A: 40

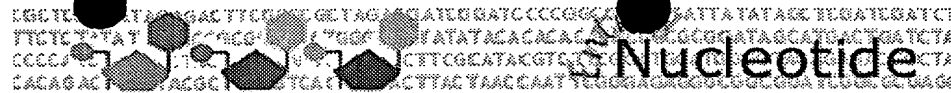
X1: 15 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 39 (21.7 bits)

S2: 73 (32.7 bits)



Search for

Display Show:

History Clipboard Details

☐ 1: AF269150. Homo sapiens tran...[gi:9755050]

Links

LOCUS AF269150 3592 bp mRNA linear PRI 09-AUG-2000
DEFINITION Homo sapiens transmembrane protein TM9SF3 (TM9SF3) mRNA, complete cds.
ACCESSION AF269150
VERSION AF269150.1 GI:9755050
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

FEATURES
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LEIGFNGNRIVDVNLTSSEKVKLVNPTKIQISYSVKWKKSDVKFEDRFKYLDPSFFQ
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BASE COUNT 1026 a 604 c 815 g 1147 t
ORIGIN

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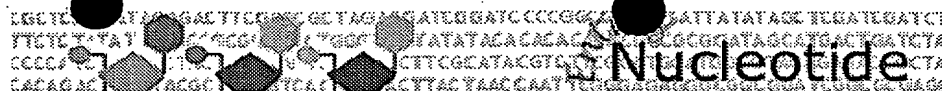
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1155)

REFERENCE
 AUTHORS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
 Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
 Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
 Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
 Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
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 Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
 Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
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 Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
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 Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,
 Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1155)

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
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 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
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 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
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 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

JOURNAL Nature 420 (6915), 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

REFERENCE 3

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AK075807.1.

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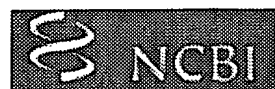
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Nucleotide

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☐ 1: AF116347. Homo sapiens SM-1...[gi:6650721]

Links

LOCUS AF116347 1804 bp mRNA linear PRI 16-OCT-2001

DEFINITION Homo sapiens SM-11044 binding protein mRNA, partial cds.

ACCESSION AF116347

VERSION AF116347.1 GI:6650721

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,

Guillaume, J.L., Camoin, L., Strosberg, A.D. and Nahmias, C.

TITLE The iodothyronine deiodinase and SM-11044 binding protein belongs to the TM9SF multispansing membrane protein superfamily

JOURNAL Gene 273 (2), 227-237 (2001)

MEDLINE 21479397

PUBMED 11595169

REFERENCE 2 (bases 1 to 1804)

AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,

Guillaume, J.L., Camoin, L., Nahmias, C. and Strosberg, A.D.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1998) Vetigen, 21 rue Sebastien Mercier, Paris 75015, France

FEATURES

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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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☐ 1: NM_067729. Caenorhabditis el...[gi:17543267]

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DEFINITION Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA.
ACCESSION NM_067729
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ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final NCBI review. The reference sequence was derived from WormBase CDS:Y41D4A.4. Fully supported by cDNA from the Worm Transcriptome Project. COMPLETENESS: full length.
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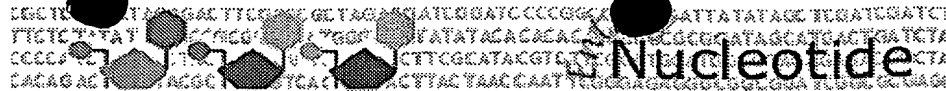
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May 20 2003 11:20:12



Search for

Display Show:

☐ 1: BC046021. Danio rerio, Simi...[gi:28278504]

LOCUS BC046021 2082 bp mRNA linear VRT 10-FEB-2003
DEFINITION Danio rerio, Similar to expressed sequence AW146116, clone
MGC:56246 IMAGE:5601580, mRNA, complete cds.
ACCESSION BC046021
VERSION BC046021.1 GI:28278504
KEYWORDS MGC.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2082)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 103 Row: 1 Column: 14.

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//

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May 20 2003 11:20:17



results of BLAST

TBLASTN 2.2.6 [Apr-09-2003]

Seq ID No. 6

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

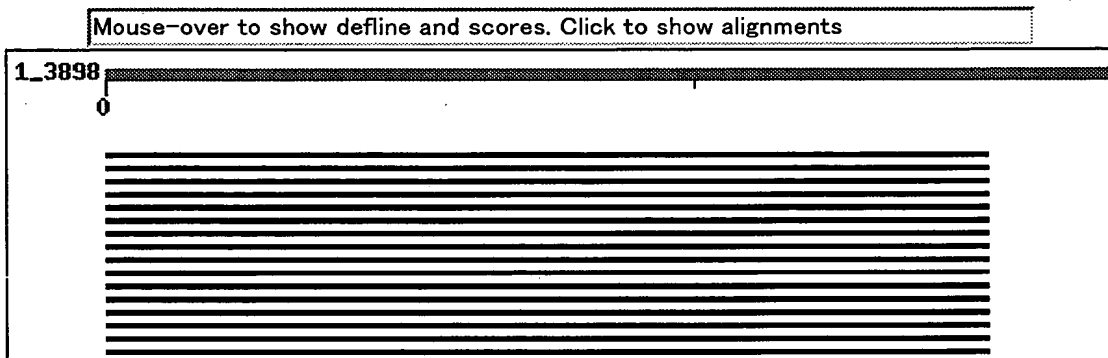
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Query=

(17 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,772,460 sequences: 8,313,506,101 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reportsDistribution of 16 Blast Hits on the Query Sequence

Sequences producing significant alignments:

	Score (bits)	E Value	
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gi 30026031 ref NM_178146.1 Mus musculus RIKEN cDNA 181007...	<u>35</u>	2.7	L
gi 26344651 dbj AK075807.1 Mus musculus 10 day old male pa...	<u>35</u>	2.7	L
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gi 18088072 gb BC020959.1 BC020959 Homo sapiens, clone MGC:...	<u>35</u>	2.7	LU
gi 9755050 gb AF269150.1 AF269150 Homo sapiens transmembran...	<u>35</u>	2.7	LU
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gi 24658498 ref NM_139722.2 Drosophila melanogaster CG1059...	<u>34</u>	3.6	L
gi 17945956 gb AY071401.1 Drosophila melanogaster RE48767 ...	<u>34</u>	3.6	LU

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|9755048|gb|AF269149.1|AF269149 Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds
Length = 234

Score = 34.7 bits (78), Expect = 2.7
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☐ >gi|6650721|gb|AF116347.1|AF116347 Homo sapiens SM-11044 binding protein mRNA, partial cds
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Sbjct: 434 DPSFFQHR IHWF SIFN 481

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cds
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MGC:56246 IMAGE:5601580, mRNA, complete cds
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Sbjct: 823 DPNFFQHRHHVFSIFN 870

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Length = 2662

Score = 34.3 bits (77), Expect = 3.6
Identities = 14/16 (87%), Positives = 14/16 (87%)
Frame = +1

Query: 1 DPXFFQHRHHVFSIFN 16
DP FFQHRHH FSIFN
Sbjct: 823 DPNFFQHRHHVFSIFN 870

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: May 30, 2003 12:03 AM

Number of letters in database: -276,428,487

Number of sequences in database: 1,772,460

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Gapped		
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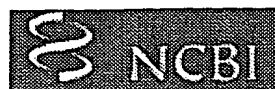
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Gap Penalties: Existence: 11, Extension: 1

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Number of Sequences: 1772460

Number of extensions: 713471
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Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 29804
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
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X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 38 (21.6 bits)
S2: 73 (32.7 bits)



NCBI Nucleotide

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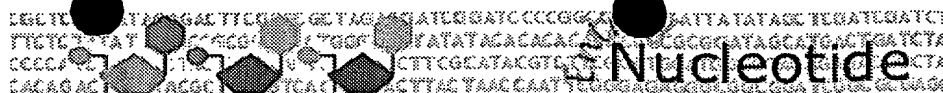
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☐ 1: AF269149. Gallus gallus tra...[gi:9755048]

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DEFINITION Gallus gallus transmembrane protein TM9SF3 (TM9SF3) mRNA, partial cds.
ACCESSION AF269149
VERSION AF269149.1 GI:9755048
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 234)
AUTHORS Gong, T. W., Hegeman, A. D., Shin, J. J., Adler, H. J., Raphael, Y. and Lomax, M. I.
TITLE Identification of genes expressed after noise exposure in the chick basilar papilla
JOURNAL Hear. Res. 96 (1-2), 20-32 (1996)
MEDLINE 96414275
PUBMED 8817303
REFERENCE 2 (bases 1 to 234)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 234)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA
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Search Nucleotide for

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☐ 1: NM_178146. Mus musculus RIKE...[gi:30026031]

LOCUS 1810073M23Rik 1155 bp mRNA linear ROD 18-MAY-2003
DEFINITION Mus musculus RIKEN cDNA 1810073M23 gene (1810073M23Rik). mRNA.
ACCESSION NM_178146
VERSION NM_178146.1 GI:30026031
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932

REFERENCE
AUTHORS 2 (bases 1 to 1155)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusica, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
REFERENCE
AUTHORS 3
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AK075807.1.

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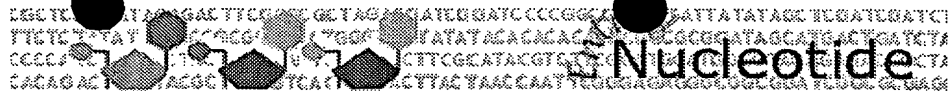
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Links

☐ 1: AF116347. Homo sapiens SM-1...[gi:6650721]

LOCUS AF116347 1804 bp mRNA linear PRI 16-OCT-2001
DEFINITION Homo sapiens SM-11044 binding protein mRNA, partial cds.
ACCESSION AF116347
VERSION AF116347.1 GI:6650721
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
REFERENCE 1 (bases 1 to 1804)
AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J. L., Camoin, L., Strosberg, A. D. and Nahmias, C.
TITLE The iodocyanopindolol and SM-11044 binding protein belongs to the
TM9SF multispinning membrane protein superfamily
JOURNAL Gene 273 (2), 227-237 (2001)
MEDLINE 21479397
PUBMED 11595169
REFERENCE 2 (bases 1 to 1804)
AUTHORS Sugawara, T., Lenzen, G., Simon, S., Hidaka, J., Cahen, A.,
Guillaume, J. L., Camoin, L., Nahmias, C. and Strosberg, A. D.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-1998) Vetigen, 21 rue Sebastien Mercier, Paris
75015, France
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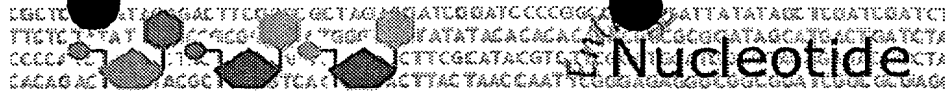
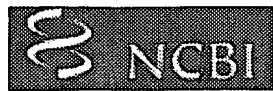
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1801 aaaa

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☐ 1: NM_067729. Caenorhabditis el...[gi:17543267]

LOCUS 4C515 1743 bp mRNA linear INV 22-NOV-2002
DEFINITION Caenorhabditis elegans transmembrane protein TM9SF3 (66.6 kD), mRNA.
ACCESSION NM_067729
VERSION NM_067729.1 GI:17543267
KEYWORDS
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final NCBI review. The reference sequence was derived from WormBase CDS:Y41D4A.4. Fully supported by cDNA from the Worm Transcriptome Project.
COMPLETENESS: full length.

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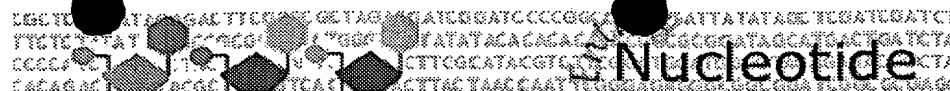
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ACCESSION AF269150
VERSION AF269150.1 GI:9755050
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REFERENCE 1 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3592)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

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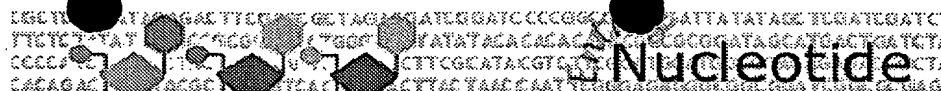
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3143)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Evolution of the TM9 Super Family of Membrane Spanning Proteins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3143)
AUTHORS Warner, S. J. and Lomax, M. I.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical Center Drive, Ann Arbor, MI 48109-0648, USA

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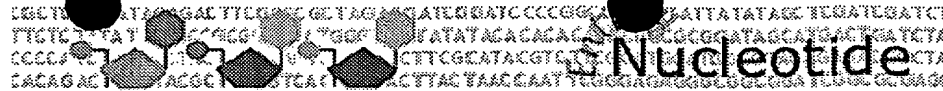
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☐ 1: AY071401. Drosophila melano...[gi:17945956]

LOCUS AY071401 2662 bp mRNA linear INV 20-DEC-2001
DEFINITION Drosophila melanogaster RE48767 full length cDNA.
ACCESSION AY071401
VERSION AY071401.1 GI:17945956
KEYWORDS FLI_CDNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2662)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Rubin, G. M.
and Celniker, S.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.
FEATURES
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BASE COUNT 672 a 651 c 613 g 726 t

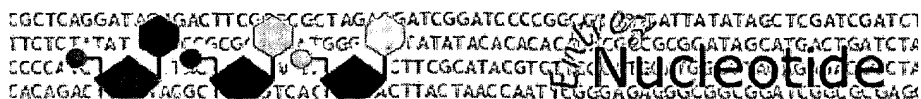
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May 20 2003 11:20:17



 1: Z28655. HSB72F051 STRATAG...[gi:434270]

Links

dbEST Id: 38740
EST name: HSB72F051
GenBank Acc: Z28655
GenBank gi: 434270

Clone Id: 72F05
DNA type: cDNA

PolyA Tail: Unknown

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Entry Created: Dec 14 1993
Last Updated: Dec 14 1993

strand(-), single read

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Lib Name:      STRATAGENE Human skeletal muscle cDNA library, cat. #936215.
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Sex:           Female
Organ:         leg muscle
Tissue type:   skeletal muscle
Develop. stage: 19 years
Vector:        Lambda ZAPII
Description:    Tissue from female, 19 years old, normal leg muscle. Cloning
                vector is Lambda ZAPII, in vivo excision from lambda ZAPII
                to pBluescript SK(+). Genexpress library reference is B.

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Name: Genethon
Lab: Genexpress-Genethon
Institution: Genethon Centre de recherche sur le Genome Humain
Address: 1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
E-mail: genexpress@genethon.fr

Medline UID: 95277534

Title: IMAGE: molecular integration of the analysis of the human genome and its expression
Authors: Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C., Tessier,A.
Citation: C. R. Acad. Sci. III, Sci. Vie 318 (2): 263-272 1995

MAP DATA

Revised: July 5, 2002.

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